

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2003, 09:30:59 ; Search time 4316 seconds
(without alignments)
12805.463 Million cell updates/sec

Title: US-09-494-297-1
2274
Perfect score: 1 atgaaaaacaagttcc.....ggataagaacaacgactag 2274
Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.2	3.1	1101	29	CNS00396
2	69.4	3.1	1200	13	AX437758 BX437758
3	66.8	2.9	1201	13	BX462660 BX462660
4	65.2	2.9	960	13	BX346155 BX346155

Result No.	Score	Query Match	Length	ID	Description
5	65.2	2.9	1201	9	AL536104
6	64.2	2.8	687	12	BM169292
7	64.2	2.8	1056	13	BX415058
8	63.8	2.8	1169	13	BX448176
9	63.2	2.8	395	12	BM166601
10	63.2	2.8	964	13	BX341256
11	62.2	2.7	1201	13	BX439779
12	61.8	2.7	1098	13	BX377526
13	61.6	2.7	1044	13	BX415231
14	61.4	2.7	506	12	BM170012
15	61.4	2.7	770	12	BM169947
16	61.4	2.7	1101	29	CNS00EVL
17	61.1	2.7	1201	29	CNS0167M
18	60.8	2.7	1201	13	BX376097
19	60.6	2.7	998	13	BX436885
20	60.4	2.7	512	12	BM163047
21	60.4	2.7	999	13	BX380865
22	60.2	2.6	823	28	A2687380
23	60.2	2.6	1092	29	CNS020K7
24	60.2	2.6	1101	29	CNS01219
25	60.2	2.6	994	13	BX414650
26	60.0	2.6	1101	29	CNS00EPO
27	59.8	2.6	1008	13	BX398691
28	59.4	2.6	549	12	BM161900
29	59.4	2.6	747	12	BM169149
30	59.2	2.6	1032	29	CNS020IP
31	58.6	2.6	762	12	BM166229
32	58.6	2.6	879	29	CNS01JRG
33	58.6	2.6	1007	29	CNS06X9S
34	58.6	2.6	1200	29	CNS016CO
35	58.4	2.6	600	12	BM160720
36	58.2	2.6	932	9	AL514901
37	57.8	2.5	743	12	BX446581
38	57.8	2.5	891	28	A2683582
39	57.4	2.5	652	29	CNS03HOU
40	57.4	2.5	1101	29	CNS000B8
41	57.4	2.5	1201	9	AL514421
42	57.2	2.5	1201	9	AL536104
43	57.2	2.5	1124	13	BX436282
44	57.2	2.5	1200	13	BX415878
45	57.2	2.5	1201	13	BX446296

ALIGNMENTS

RESULT 1
CNS00396/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RP1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL063921
VERSION
AL063921.1 GI:4941778
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osega and Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Db	770	TAMWTATTTT	TTTWWANAAGATDRKAAAAA	MMWTTTWTAAAAAAAT	TTTWWAGARAAAT	825
QY	1924	AAAACAGAT	TAACAACCACTCGAATTTTAAGATG	TGTAAGCAGCAACCATT	TAATTTAAACAT	1983
Db	830	TTAAWMAAAAAA	AAAAAARMAATATATTTATTTATAT	TAATAKARAAAAAT	TAATTAARAA	889
QY	1984	GGGGAAGCTT	TAACACTTCAAGCTTACGACAGAT	TATCTTCTTGTAAGGAACA	2043	
Db	890	RRMGAAAAA	AAAAAATAAAAAAMWTTWTATAAAAA	AMATTTWMAWRAAARMAWMAA	949	
QY	2044	GATTCCTGAAGC	TTAAGCTTAAGCTTAATATAGCCAG	ACAGCAATGCTACAGTTCA	2103	
Db	950	GAAARAGMAA	MAAATTTTATTTTAAATATRRMAA	AAAAAMWTTTWTWRAAAMWMDTTT	1009	
QY	2104	AAACAGGAAT	TAACAGTATGACACACTTCTTTG	AAATAATTAAGAG	2154	
Db	1010	TATWTATWT	AMTATAGMAAATATADATWRAT	TATTWADAARAAAGAMTAK	1060	
RESULT 3						
LOCUS	BX462660/c	1201 bp	mRNA	linear	EST-22-MAY-2003	
DEFINITION	BX462660 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA					
ACCESSION	BX462660					
VERSION	BX462660.1	GI:31031442				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1. (bases 1 to 1201)					
TITLE	L.I.W.B., Gruber,C., Jesse,J., and Polayes,D.					
JOURNAL	Full-length cDNA libraries and normalization					
COMMENT	Unpublished					
FEATURES	<p>Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3370.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DH005DE01Q1&cluster=3370.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DH005DE01Q1.</p>					
SOURCE	Location/Qualifiers					
	1. 1201					
	/organism="Homo sapiens"					
	/mol_type="mRNA"					
	/db_xref="taxon:9606"					
	/clone="CS0DH005YJ02"					
	/issue_type="T CELLS (JURKAT CELL LINE)"					
	/cell_line="JURKAT CELL LINE"					
	/clone_id="Homo sapiens T CELLS (JURKAT CELL LINE)"					
	/note="Vector: pCMVSPORT 6, 1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."					
BASE COUNT	277 a 121 c 246 g 460 t 97 others					
ORIGIN						
Query Match	2.9%: Score 66.8; DB 13; Length 1201;					
Best Local Similarity	38.1%: Pred. No. 0.08; 268; Indels 0; Gaps 0;					
Matches 196; Conservatively 51; Mismatches 268; Indels 0; Gaps 0;						
QY	1753	GAAAGATTAGT	TATATATTCGTATGAGATAAAAAGAA	GTATATACCTGTAACAT	1812	
Db	1177	GRGRDRKGGG	GGGAAAAAARAAAAAATTAATTA	AAAAAATTTTNGAAMARAA	1118	
QY	1813	AATTTAACTT	GACAAAAACGGTGATCGTTTACCTG	TGCACAGACTAAAGATTTCCAT	1872	

[illegible]

[illegible]

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/mol_type="mRNA"
/db_xref="taxon:73239"
/clone="pICP070"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_lib="PyBS"
/note="Vector: PAD-GAL4: At 20-25% parasitemia, blood was
collected from BALB/Cby mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcrystalline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HybridZap arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (PAD-GAL4) was
excised from the HybridZap vector and plasmid DNA
isolated."
BASE COUNT      424 a      23 c      131 g      109 t
ORIGIN

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Query Match 2.8%; Score 64.2; DB 12; Length 687;

Best Local Similarity 49.5%; Pred. No. 0.23;

Matches 165; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

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1851 TGACAGAACTTAAGATTTCCATTTTGAATTAATAAATATAGCAAGATTCT 1910
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
109 TGATGAACTTAATAATGATGATTAATAAATGATGATTAATAATGATGATTA 168
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1911 TTCTCAACTCTTAAACAGATAAACAACCTCGAATTTAAGATGTTAAAGCAAC 1970
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
169 TGATGAAAGAAAAAAGACGAAGAAAAAAGACGAAGTAAATAATGATGAAGAAA 228
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1971 TAATTTAAACATGGGAAAGTTTACACCTTCAAGGTTTACCAGAGTTATTCT 2030
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
229 AGACGAAGTAAATAATGATGATGATGATGATGATGATGATGATGATGATG 288
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2031 TGCTAAGAAACAGATTTCTGAAGCTAATAGGTTAAGTTATGACCAAGATG 2090
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
289 TGACGAAGTAAATAATGATGATGATGATGATGATGATGATGATGATGATG 348
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2091 TGCTACAGTTTCAAAAACAGAAATACAAAGTATGATGATGATGATGATGAT 2150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
349 TGATGAAAGTAAATAATGATGATGATGATGATGATGATGATGATGATGAT 408
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2151 AGAGCTGTGTTCTCTACAGAGTTGATCAAAA 2183
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
409 TGACGAAGTAAATAATGATGATGATGATGATGATGATGATGATGATGATG 441
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 7
LOCUS      BX415058      1056 bp      mRNA      linear      EST 15-MAY-2003
DEFINITION BX415058 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP004YG19
ACCESSION  BX415058
VERSION     BX415058
KEYWORDS    3-PRIME, mRNA sequence.
SOURCE      BX415058.1 GI:30767520
ORGANISM    Homo sapiens (human)
HOMOLOGUES  Homo sapiens
REFERENCE   1 (bases 1 to 1056)
AUTHORS     Li, M.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
COMMENT     Contact: Genoscope

```

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Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP004AD10NP1.
FEATURES
Source
1. 1056
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP004YG19"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the
pCMVSPORT 6 vector.
Library was not normalized."
BASE COUNT      454 a      53 c      56 g      318 t      175 others
ORIGIN

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Query Match 2.8%; Score 64.2; DB 13; Length 1056;

Best Local Similarity 33.9%; Pred. No. 0.23;

Matches 186; Conservative 91; Mismatches 263; Indels 9; Gaps 1;

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1694 ATTCTTTATTCGGAATACATATATATCATCTCTTATGCAAGTCAGTCATCCAG 1753
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
483 AATTTTATATATATATATATATATATATATATATATATATATATATATATAT 542
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1754 AAGTATTTGATATATATATATATATATATATATATATATATATATATATATAT 1813
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
543 AATAATATATATATATATATATATATATATATATATATATATATATATATATAT 602
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1814 ATTTACATTTGAGAAAAAGCTGCTGTTAGCTGTGACAGACTAAAGATTTCCATT 1873
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
603 TTTCGAATAATGTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 662
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1874 TTGAATATGATTTAAATAATATATAGCAAGATTCCTTCAACCTGTTAAACAGATA 1933
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
663 DATWAAATATATATATATATATATATATATATATATATATATATATATATATAT 722
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1934 AACAACCTCGAATTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1993
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
723 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 782
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1994 TAACACTTCAAGGTTTACCAAGGTTTATCTTACCTGCAAGCAACAGATTCTGAAG 2053
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
783 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 842
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2054 GCTATACGTTTAAAGTTATATAGCCAGAGTACGATGATGATGATGATGATGAT 2113
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
843 WWWWAAATATATATATATATATATATATATATATATATATATATATATATATAT 902
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2114 TAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2164
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
903 AAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 962
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2165 CTACAGAGTATGATCAAAAGATCAATGCTATGATGATGATGATGATGATGATGAT 2224
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
963 TAGGAGGCTTTWAAAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1022
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2225 GTTTGGGGA 2233
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1023 KTKKKKKRA 1031
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 8
LOCUS      BX448176/c      1169 bp      mRNA      linear      EST 22-MAY-2003
DEFINITION BX448176 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
CSODM006Y18 3-PRIME, mRNA sequence.

```

Accession	Version	Keywords	Source	Organism	Reference	Authors	Title	Journal	Comment
BX448176	1	GI:31023901		Homo sapiens (human)					
BX448176.1	1	GI:31023901		Homo sapiens					
EST.				Homo sapiens					
ORGANISM				Homo sapiens					
REFERENCE				Mammalia: Eutheria: Chordata: Craniata: Vertebrata: Euteleostomi;					
AUTHORS				Lt.W.B., Gruber,C., Jesse,J., and Polayes,D.					
TITLE				Full-length cDNA libraries and normalization					
JOURNAL				Unpublished					
COMMENT				Contact: Genoscope					
				Genoscope - Centre National de Sequencage					
				BP 191 91006 EVRY cedex - France					
				Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr					
				Library was constructed by Life Technologies, a division of					
				Invitrogen. This sequence belongs to sequence cluster 1232.f For					
				more information about this cluster, see					
				http://www.genoscope.cns.fr/					
				cgl-bin/cluster.cgi?seq=CS0AM006DC09NP1&cluster=1232.f. Contact :					
				Feng liang Email : fliang@life.techn.com URL :					
				http://fulllength.invitrogen.com/ Invitrogen Corporation 1600					
				Faraday Avenue Genoscope sequence ID : CS0AM006DC09NP1.					
FEATURES				Location/Qualifiers					
Source				1..1169					
				/organism="Homo sapiens"					
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				/clone="CS0DM006YP18"					
				/tissue_type="FETAL LIVER"					
				/dev_stage="fetal"					
				/clone_1lb="Homo sapiens FETAL LIVER"					
				/note="Organ: Liver; Vector: pCMVSPORT_6; 1st strand cDNA					
				was primed with a NotI-Oligo(dT) primer. Five prime end					
				enriched, double-strand cDNA was digested with Not I and					
				cloned into the Not I and EcoRV sites of the pCMVSPORT 6					
				vector. Library was not normalized."					
BASE COUNT				258 a 127 c 167 g 437 t 180 others					
ORIGIN									
Query Match				2.8%; Score 63.8; DB 13; Length 1169;					
Best Local Similarity				37.4%; Pred. No. 0.27; Mismatches 317; Indels 0; Gaps 0;					
Matches				222; Conservative 54; Mismatches 317; Indels 0; Gaps 0;					
OY				1615 AATGATAGTACTTTAGCAGTTCCTAAATCTTGTGAGATAGCGCTCAAGATAGTAATCTT					
DB				845 AMGACATCTTCTTACATATGATGATCTTMMCCATCTACCTCTCCACCATCTCATTTAA					
OY				1675 CCACAGCTAAGTACGACCTGTTCTTTATTCGGAATTAACAATTAATTCATCTCTTAT					
DB				785 ATATATATATATTTAAACAGCTCTTACCTCACTATTTAAACAAATTTAAACAAACCTT					
OY				1735 GGAATCTGCTGGACCTCCGAAGATTTATTTATCTGATTTGATTTGATTTGATTTGAT					
DB				725 AAAAATAATATTAACACATCACTATTTTTCAGATCTTTTGTGCTGAGACATTTAAATAT					
OY				1795 GTTATACCTGATCACTATTTTAACTTTGAGAAAAACGCTGACGTTTACCTGCTGAC					
DB				665 TRACCTATCAAGAGAACATAGAAAAAGTGTGATCTTTCACAGATTTTGCATGTGAC					
OY				1855 AGAATCAAGATTTCCATTTTGAATTTGAATTTAAATTTAAATTTAAATTTAAATTT					
DB				605 ACCCTTATATATATTTTCCCAATTTTAACTCTATTTTAAATTTTAAATTTTAAATTT					
OY				1915 CAACTGTTTAAACAGATTTAAACAACTCGAATTTTAAAGTTGTAAGCAACCATTAAT					
DB				545 AAAAATAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAAT					
OY				1975 TTTAAACATGCGGAA					

<p>Db</p> <p>425 MAAAAAAAAAGCGCCCTATWTWCTATATAAAAAAAMTAAAAAACAAAAA 2095 ACAGTTTCAAAAACAGCATTAACAAGTGATGAGACACTTGGTTTTGA Db MAAMAANAAMAAATVMMMAAAAACABRAGGTCCBMACAAAAAMAA 365 MAAMAANAAMAAATVMMMAAAAACABRAGGTCCBMACAAAAAMAA Oy 2155 CCTGTGTCTCCTACAGAGCTGCATCAAAAGATCAATGCTATCA Db 305 MAAAAAMTAAAMAAAAAAAARAAATCTATRRAAAACTGGGAATGT </p>	<p>RESULT 9</p> <p>BMI66601 395 bp mRNA linear EST 04-DEC-2001 Locus ESR569124 PYBS Plasmodium yoelii yoelii cDNA clone PYCNU37 5' end, Definition RNA sequence. Accession BMI66601 GI:17299833 Keywords EST.</p> <p>ORGANISM</p> <p>Plasmodium yoelii yoelii Plasmodium yoelii yoelii Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. REFERENCE</p> <p>1 (bases 1 to 395) Carlton,D.M., Baily,T.M., Long,C.A., Bergman,L.W., Valdya,A.B., Fraser,C.M. and Carucci,D.J. Plasmodium yoelii EST project at TIGR Unpublished AUTHORS</p> <p>Contact: Jane Carlton Parasite Genomics Group The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-530-9319 Fax: 301-838-0208 Email: carlone@tigr.org For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html Seq primer: ADP.</p> <p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>	<p>FEATURES</p> <p>SOURCE</p> <p>Location/Qualifiers</p> <p>1..395</p> <p>/organism="Plasmodium yoelii yoelii"</p> <p>/mol_type="mRNA"</p> <p>/strain="17XL"</p> <p>/db_xref="taxon:73239"</p> <p>/clone="PYCNU37"</p> <p>/dex_stage="asexual blood stages"</p> <p>/lab_host="E. coli XL-1 Blue"</p> <p>/clone_1lb="PyBS"</p> <p>/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBy mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."</p>	<p>BASE COUNT</p> <p>232 a 80 g 64 t</p> <p>ORIGIN</p> <p>Query Match 2.8%; Score 63.2; DB 12; Length 395; Best Local Similarity 50.7%; Pred. No. 0.34; Indels 0; Matches 152; Conservative 0; Mismatches 148; Gaps 0;</p>
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D6 534 AAAAATAAAATTTTTTTTAAAATTAAAAATTAAATTAATTTTATAATA 593

Matches 194; Conservative 76; Mismatches 276; Indels 2; Gaps 1;

